



# Sequence Listing

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Baker Kevin P.  
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Desnoyers, Luc  
Eaton, Dan  
Ferrara, Napoleon  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J  
Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.

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Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
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tgagcttctg gtgcnttttg gctctaattc tggccacaca gagaancagt 100  
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
ggcccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350  
tctgtttcgt gatgttttgg acacccaacg tgtctgngaa aatcttgata 400  
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450  
gcgggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500  
ccgggtgggt gatgacactg aagaaaacct tcgtc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
tgacggaatc ccgggctggg tatcctgggt tngacaagat aaacccccag 50  
caanaaattg gggagcaggg caaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150  
gttttgagca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgacagaa ntttgngntg ttcctttgcg gatcttctcc 250  
tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400  
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

<400> 10  
tattccagcgt tccgggtcacg gggagggcgc atntcacggg gtggctgang 50  
aactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100  
cgctctcatc gccagcctng tggctcctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattctcttc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttccgcca cggagttc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtcc actccgatga tgtc 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

<400> 18  
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50  
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100  
ctctgcccc tgcatcctgt gcagctgctg ccccgccagc cgcaactcca 150



ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350  
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400  
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450  
ttaagttcct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500  
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggtcctt 550  
cctcttcctc ctcatccagc tgggtgctgt catcgacttt gcgcactcct 600  
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650  
tacgcaggcc tcttcttctt cactctcctc ttctacttgc tgcgatcgc 700  
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750  
agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800  
atcgctgctg tcctgcccaa ggtccaggac gccagccca actcgggtct 850  
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900  
ccctatccag tatccctgaa cagaaatgca acccccattt gccaacccag 950  
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000  
gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050  
tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150  
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactccttc ttccacttct gcctggtgct ggctcactg 1250  
cacgtcatga tgacgctcac caactggtac aagcccggtg agaccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
cagggctgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400  
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450  
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500  
caccaatcag ccaggctgag cccccacccc tgcccagct ccaggacctg 1550  
cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650  
 cctcttcctt cccctcctcc ctgttgcca tactcagcat ctcggatgaa 1700  
 agggctccct tgctctcagg ctccacggga ggggggctgc tggagagagc 1750  
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800  
 tggtcacgtc cccagggga cctgcccc ttctggact tcgtgcctta 1850  
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900  
 a 1901

<210> 19  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	1	5	10	15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	20	25	30	
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	35	40	45	
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly	50	55	60	
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75	
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90	
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105	
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120	
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135	
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150	
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165	
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180	

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 20  
gccgcctcat cttcacgttc ttcc 24  
  
<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 21  
tcattccagct ggtgctgctc 20  
  
<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 22  
ctttttccac ttctgcctgg 20  
  
<210> 23  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 23  
cctgggcaaa aatgcaac 18  
  
<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 24  
caggaatgta gaaggcacc acgg 24  
  
<210> 25  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
tggcacagat cttcacccac acgg 24

<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
tgtccatcat tatgtgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50  
ttaacctggg tcaaatgcac ggattctcac ctctgacagt tacgctctcc 100  
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150  
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250  
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
cccagagccc tattaccgag aatctggatg ggaccgcctc cgggagctgt 350  
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550  
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaa ctgcagtgtt 600  
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650  
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggagtcctt 700  
tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750  
agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900  
 cctccctgag aaaattgaaa gtagttttacg ggaagatgaa cctgagaatg 950  
 atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000  
 atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050  
 gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100  
 tctttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150  
 tggcttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200  
 gtactctcac ttactttatc cttaaattta aatacatact tatgtttgta 1250  
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350  
 t 1351

<210> 28  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Glu Val Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
 1 5 10 15  
 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
 20 25 30  
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val  
 35 40 45  
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu  
 50 55 60  
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala  
 65 70 75  
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val  
 80 85 90  
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile  
 95 100 105  
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val  
 110 115 120  
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly  
 125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50  
 ctattaccgc gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttcgttcattg gctggcgccc aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 262, 330, 371  
<223> unknown base

<400> 30  
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50  
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100  
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
tcgtacagtt acgctctccc 20

<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgcccgc cgcgcgcgcgc cgcgcgactg cagccccagg ccccggcccc 50

ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100

gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150

tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgccct caacctgctt tacaccttg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg cttegggctg atttccagtc 300

tccgagtggc cgcgtgggc attgcagtgg gcattcttct gtccctgatt 350

gcttttagtg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400

tttttatatg attattctgt tacttgatt tattgttcag tttctgtat 450

cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500

gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaacct aatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650

gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagaccc ccgcgcgaat cctagtgcatt tcctttgatg agaaaacaag 800

gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850

taagctccat ttgccagttt aaggaaggaa aactatctg gaaaagtacc 900

ttattgatag tggaattata ttttttact ctatgtttct ctacatgttt 950

ttttctttcc gttgctgaaa aatatttgaa acttggtggtc tctgaagctc 1000

ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050

cctttcttag catttttacc tgcagaaaaa ctttgatgg taccactgtg 1100



Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	110	115	120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	125	130	135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	140	145	150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	155	160	165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	170	175	180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	185	190	195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							200		

<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

<400> 37  
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 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300  
 gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350  
 gatcctgggt gtttggtgta cctacagata caggaaccag 390

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27

<223> unknown base

<400> 38

aatcccaa at tccccaat ttttggnc ttttagggaa gatgtgtgt 50  
ggtaaaaaagt gtaggtataa aaatgataat ttactttag tcttttatga 100  
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttaa 150  
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200  
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500  
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550  
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgtttagc ccctgaaacc aggagcaaca gggnnacagct tcctggaggt 100  
tggttggtcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200  
tggtctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40  
 acccacgtct gcgttgctgc c 21

<210> 41  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 41  
 gagaatatgc tggagagg 18

<210> 42  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 42  
 aggaatgcac taggattcgc gcgg 24

<210> 43  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 43  
 ggccccaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44  
 <211> 2061  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
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 cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200  
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gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400  
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agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300  
tctgctgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350  
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 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgccct 2000  
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050  
 ttgtagccta a 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
 20 25 30  
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150  
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
 155 160 165  
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
 170 175 180  
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcagcgc caattctc 18

<210> 48



<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
cccacgcgtc cgccacgcg tccgccacg ggccgccca cgcgtccggg 50  
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100  
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
gtgtaacagg accttggaag ggggatgtga atcttcctg cacctatgac 250  
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300  
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350  
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gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550  
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 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
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 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
                     20                    25                    30  
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
                     35                    40                    45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
                     50                    55                    60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
                     65                    70                    75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
                     80                    85                    90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
                     95                    100                    105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
                     110                    115                    120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
                     125                    130                    135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
                     140                    145                    150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
                     155                    160                    165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
                     170                    175                    180  
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
                     185                    190                    195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
				200					205					210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
				215					220					225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
				230					235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
				245					250					255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
				260					265					270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
				275					280					285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
				290					295					300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
				305					310					315
Val	Tyr	Glu	Ala	Ala	Arg									
				320										

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 53  
 tatccctcca attgagcacc ctgg 24

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 54  
 gtcggaagac atcccaacaa g 21

<210> 55  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgcccgggag cccatctgcc cccaggggca cggggcgcgcg gcccggtcc 50

cgcccggcac atggtgcag ccacctcgcg cgcaccccga ggcgccgcgc 100

ccagctcgcc cgaggtcgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaacctg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

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cgataatgaa gggaacaaaa aagtggatgat cacttactcc agtcgtcatg 400

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aatttcctgg caggagatgc ctcccttgag attgaacctc tgaagcccag 500

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ctaactctac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000  
aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050  
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cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150  
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 agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250  
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 tagaaagggg gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350  
 cgggcatggg gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400  
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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro

170										175				180			
Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu			
				185					190					195			
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala			
				200					205					210			
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val			
				215					220					225			
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly			
				230					235					240			
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu			
				245					250					255			
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro			
				260					265					270			
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val			
				275					280					285			
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly			
				290					295					300			
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln			
				305					310					315			
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr			
				320					325					330			
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro			
				335					340					345			
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro			
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtgcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val
				575					580					585
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe
				590					595					600
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
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Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 65  
 gtagcagtgc acatggggtg ttgg 24

<210> 66  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 66  
 accgcacatc ctccagtctct gtcc 24

<210> 67  
 <211> 50  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 67  
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<210> 68  
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 <212> DNA  
 <213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45

Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



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Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly	65		70		75
Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala	80		85		90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	95		100		105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe	110		115		120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly	125		130		135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr	140		145		150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe	155		160		165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys	170		175		180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala	185		190		195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg	200		205		210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu	215		220		225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His	230		235		240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala	245		250		255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile	260		265		270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His	275		280		285
Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg	290		295		300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr	305		310		315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu	320		325		330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala					

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Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala	350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr	365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr	380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val	395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe	410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg	425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp	440	445	450

Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

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<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

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<400> 72

cgttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<212> PRT

<213> Homo sapiens

<400> 74

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Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
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Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
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Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
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Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
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Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
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Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
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Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
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Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

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Glu	Ala	Ala	Glu	Ser	Asn	Arg	Glu	Arg	Gly	Gln	Gly	Gln	Glu	Pro
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<211> 483

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<213> Homo sapiens

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<223> unknown base

<400> 75

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<212> PRT

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Thr	Ser	Met	Pro	Glu	Ala	Thr	Ala	Ala	Glu	Thr	Thr	Lys	Pro	Ser
				35					40					45

Asn	Ser	Ala	Leu	Gln	Pro	Thr	Ala	Gly	Leu	Leu	Val	Val	Leu	Leu
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Ala	Leu	Leu	His	Leu	Tyr	His
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<212> PRT

<213> Homo sapiens

<400> 90

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				20					25				30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
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Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly		125	130	135
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys		140	145	150
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu		155	160	165
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu		170	175	180
Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser		185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile		200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro		215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val		230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser		245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp		260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser		275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly		290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala		305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn		320	325	330

Asn Phe Asp Asp Thr Ile Ala Glu Gly	Ile Thr Phe Ile Lys Phe
335	340 345
Tyr Ala Pro Trp Cys Gly His Cys Lys	Thr Leu Ala Pro Thr Trp
350	355 360
Glu Glu Leu Ser Lys Lys Glu Phe Pro	Gly Leu Ala Gly Val Lys
365	370 375
Ile Ala Glu Val Asp Cys Thr Ala Glu	Arg Asn Ile Cys Ser Lys
380	385 390
Tyr Ser Val Arg Gly Tyr Pro Thr Leu	Leu Leu Phe Arg Gly Gly
395	400 405
Lys Lys Val Ser Glu His Ser Gly Gly	Arg Asp Leu Asp Ser Leu
410	415 420
His Arg Phe Val Leu Ser Gln Ala Lys	Asp Glu Leu
425	430

<210> 91  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 91  
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<210> 92  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 92  
 ccaagccaac acactctaca g 21

<210> 93  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 93  
 aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
 <211> 23



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaagg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
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aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100  
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150  
atttcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200  
agaggggaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaag 250  
gagaactggg tgatatggga gatcaggga atattggcaa gactggggcc 300  
attgggaaga agggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350  
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ttgttggaaca actggatatt agtattgctc ggctcaagac atctatgaag 450  
tttgtcaaga atgtgatagc agggattagg gaaactgaag agaaattcta 500  
ctacatcgtg caggaagaga agaactacag ggaatcccta acccactgca 550  
ggattcgggg tggaatgcta gccatgcca aggatgaagc tgccaacaca 600  
ctcatcgctg actatgttgc caagagtggc ttctttcggg tgttcattgg 650  
cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700  
cactgcagaa ctatagcaac tggaatgagg gggaaccag cgaccctat 750  
ggtcatgagg actgtgtgga gatgctgagc tctggcagat ggaatgacac 800

agagtgccat cttacatgt actttgtctg tgagttcatc aagaagaaaa 850  
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 cagttattgt tatccatcct ttttttctg attgtactac atttgatctg 950  
 agtcaacata gctagaaaaat gctaaactga ggtatggagc ctccatcatc 1000  
 aaaaaaaaaa aaaaaa 1016

<210> 97  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 97

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Leu	Val	Leu	Phe	Leu	Leu	Gln	Ile	Gln	Ser	Leu	Gly	Leu	Asp	Ile
				20					25					30
Asp	Ser	Arg	Pro	Thr	Ala	Glu	Val	Cys	Ala	Thr	His	Thr	Ile	Ser
				35					40					45
Pro	Gly	Pro	Lys	Gly	Asp	Asp	Gly	Glu	Lys	Gly	Asp	Pro	Gly	Glu
				50					55					60
Glu	Gly	Lys	His	Gly	Lys	Val	Gly	Arg	Met	Gly	Pro	Lys	Gly	Ile
				65					70					75
Lys	Gly	Glu	Leu	Gly	Asp	Met	Gly	Asp	Gln	Gly	Asn	Ile	Gly	Lys
				80					85					90
Thr	Gly	Pro	Ile	Gly	Lys	Lys	Gly	Asp	Lys	Gly	Glu	Lys	Gly	Leu
				95					100					105
Leu	Gly	Ile	Pro	Gly	Glu	Lys	Gly	Lys	Ala	Gly	Thr	Val	Cys	Asp
				110					115					120
Cys	Gly	Arg	Tyr	Arg	Lys	Phe	Val	Gly	Gln	Leu	Asp	Ile	Ser	Ile
				125					130					135
Ala	Arg	Leu	Lys	Thr	Ser	Met	Lys	Phe	Val	Lys	Asn	Val	Ile	Ala
				140					145					150
Gly	Ile	Arg	Glu	Thr	Glu	Glu	Lys	Phe	Tyr	Tyr	Ile	Val	Gln	Glu
				155					160					165
Glu	Lys	Asn	Tyr	Arg	Glu	Ser	Leu	Thr	His	Cys	Arg	Ile	Arg	Gly
				170					175					180
Gly	Met	Leu	Ala	Met	Pro	Lys	Asp	Glu	Ala	Ala	Asn	Thr	Leu	Ile
				185					190					195
Ala	Asp	Tyr	Val	Ala	Lys	Ser	Gly	Phe	Phe	Arg	Val	Phe	Ile	Gly

	200		205		210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn					
	215		220		225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser					
	230		235		240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly					
	245		250		255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys					
	260		265		270
Glu Phe Ile Lys Lys Lys Lys					
	275				

<210> 98  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

<400> 98  
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<210> 99  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 99  
 gatgatggag gctccatacc tcag 24

<210> 100  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 100  
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<210> 101  
 <211> 2574  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
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gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150  
gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200  
agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250  
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 catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala		35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu		50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp		65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys		80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro		95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu		110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser		125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala		140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp		155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala		170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe		185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro		200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro		215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg		230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His		245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu		260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met		275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly		290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro		305	310	315

Val	Pro	Gly	Tyr	Leu	Ser	Ser	Pro	Gln	Ser	Ile	Thr	Asp	Thr	Cys	320	325	330
Leu	Tyr	Ile	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Ala	Ala	335	340	345
Arg	Ile	Ser	His	Leu	Lys	Ile	Leu	Gln	Cys	Gln	Gly	Phe	Tyr	Gln	350	355	360
Leu	Cys	Gly	Val	His	Gln	Glu	Asp	Val	Ile	Tyr	Leu	Ala	Leu	Pro	365	370	375
Leu	Tyr	His	Met	Ser	Gly	Ser	Leu	Leu	Gly	Ile	Val	Gly	Cys	Met	380	385	390
Gly	Ile	Gly	Ala	Thr	Val	Val	Leu	Lys	Ser	Lys	Phe	Ser	Ala	Gly	395	400	405
Gln	Phe	Trp	Glu	Asp	Cys	Gln	Gln	His	Arg	Val	Thr	Val	Phe	Gln	410	415	420
Tyr	Ile	Gly	Glu	Leu	Cys	Arg	Tyr	Leu	Val	Asn	Gln	Pro	Pro	Ser	425	430	435
Lys	Ala	Glu	Arg	Gly	His	Lys	Val	Arg	Leu	Ala	Val	Gly	Ser	Gly	440	445	450
Leu	Arg	Pro	Asp	Thr	Trp	Glu	Arg	Phe	Val	Arg	Arg	Phe	Gly	Pro	455	460	465
Leu	Gln	Val	Leu	Glu	Thr	Tyr	Gly	Leu	Thr	Glu	Gly	Asn	Val	Ala	470	475	480
Thr	Ile	Asn	Tyr	Thr	Gly	Gln	Arg	Gly	Ala	Val	Gly	Arg	Ala	Ser	485	490	495
Trp	Leu	Tyr	Lys	His	Ile	Phe	Pro	Phe	Ser	Leu	Ile	Arg	Tyr	Asp	500	505	510
Val	Thr	Thr	Gly	Glu	Pro	Ile	Arg	Asp	Pro	Gln	Gly	His	Cys	Met	515	520	525
Ala	Thr	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Leu	Val	Ala	Pro	Val	Ser	530	535	540
Gln	Gln	Ser	Pro	Phe	Leu	Gly	Tyr	Ala	Gly	Gly	Pro	Glu	Leu	Ala	545	550	555
Gln	Gly	Lys	Leu	Leu	Lys	Asp	Val	Phe	Arg	Pro	Gly	Asp	Val	Phe	560	565	570
Phe	Asn	Thr	Gly	Asp	Leu	Leu	Val	Cys	Asp	Asp	Gln	Gly	Phe	Leu	575	580	585
Arg	Phe	His	Asp	Arg	Thr	Gly	Asp	Thr	Phe	Arg	Trp	Lys	Gly	Glu	590	595	600

Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp	605	610	615
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His	620	625	630
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His	635	640	645
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu	650	655	660
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu	665	670	675
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn	680	685	690
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu	695	700	705
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr	710	715	720
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile						725	730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 104

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 104

ggagaatgtg gccacaac 18

<210> 105

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 105  
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<210> 106  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 106  
atccacttca gcggacac 18

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 107  
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<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
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acgcgcgcat acacactcgc tctcgcttgt ccatctccct cccgggggag 150  
ccggcgcgcg ctcccacett tgccgcacac tccggcgagc cgagcccgca 200  
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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys	20	25	30	
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	35	40	45	
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys	50	55	60	
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	65	70	75	
Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp	440	445	450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met	455	460	465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly	470	475	480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser	485	490	495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe	500	505	510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg	515	520	525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser	530	535	540
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<211> 21

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

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<210> 112

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

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<213> Homo sapiens

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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114 \*

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Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln	425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
			440						445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
			455						460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
			470						475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
			485						490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
			500						505					510
Gly	Ile	Gln	Glu	Ser										
			515											

<210> 115  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 115  
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<210> 116  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 116  
 ctctctgagt gtacatctgt gtgg 24

<210> 117  
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 <212> DNA  
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 <223> Synthetic oligonucleotide probe

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 <221> unsure  
 <222> 33  
 <223> unknown base

<400> 117  
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cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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gtgcagctgc tgcgcttctt gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
				20					25					30

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40					45

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55					60



Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	
				65					70					75	
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	
				80					85					90	
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	
				95					100					105	
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	
				110					115					120	
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	
				125					130					135	
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	
				140					145					150	
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	
				155					160					165	
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	
				170					175					180	
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	
				185					190					195	
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	
				200					205					210	
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	
				215					220					225	
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	
				230					235					240	
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	
				245					250					255	
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	
				260					265					270	
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	
				275					280					285	

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaagtg 46

<210> 131  
<211> 2365  
<212> DNA  
<213> Homo sapiens

<400> 131  
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caatcaatcc aacagcatat tcggttgcac cttctacaca ctacagctat 150  
tgtaggttg cctgaggaca cgctgggcct ctgtcctgat gctgctgagc 200  
tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tctgttctt 250  
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<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	365	370	375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	380	385	390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	395	400	405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	410	415	420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	425	430	435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	440	445	450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	455	460	465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	470	475	480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	485	490	495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	500	505	510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	515	520	525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	530	535	540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	545	550	555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	560	565	570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150  
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atTTTgggga aaataaatgt cTTtgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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			20					25						30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
			35					40						45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
			50					55						60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
			65					70						75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
			80					85						90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
			95					100						105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
			110					115						120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
			125					130						135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
			140					145						150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
			155					160						165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp
			170					175						180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
			185					190						195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
			200					205						210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
			215					220						225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
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<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

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<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

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tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
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<212> DNA  
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<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143  
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<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
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<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly	35	40	45	
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly	50	55	60	
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile	65	70	75	
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln	80	85	90	
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile	95	100	105	
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro	110	115	120	
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg	125	130	135	
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn	140	145	150	

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
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Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
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Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
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Leu

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<211> 26

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<213> Artificial Sequence

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<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



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Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg	125		130		135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu	140		145		150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser	155		160		165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val	170		175		180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp	185		190		195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro	200		205		210
Asp Asp Gly Ala Lys	215				

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 103, 233  
 <223> unknown base

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 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200  
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 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
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<210> 154  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
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<210> 155  
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<400> 155

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 <212> DNA  
 <213> Homo sapiens  
 <400> 156  
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<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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				20					25					30
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
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Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60
Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120
Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135
Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150
Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165
Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180
Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195
Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210
Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225
Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240
Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys

	245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu	260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr	275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln	290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu	305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys	320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu	335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp	350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln	365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser	380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu	395	400	405
Lys Arg Val Leu Leu Gly Pro	410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
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<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
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ctgccgctat ggcagtgcc a tgggggtgct ggccttcctg gcctcggcct 300  
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cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
acccgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500  
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala	20	25	30	
Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45	
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150	



Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcgggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggt catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp
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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala
			20						25					30

Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
				35					40					45

Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
				50					55					60

Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
				65					70					75

Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
				80					85					90

Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu
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95										100					105				
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr					
				110					115					120					
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly					
				125					130					135					
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro					
				140					145					150					
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu					
				155					160					165					
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val					
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Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile					
				185					190					195					
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu					
				200					205					210					
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg					
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Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu					
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Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr					
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Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly					
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Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg					
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Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala					
				290					295					300					
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val					
				305					310					315					
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu					
				320					325					330					
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro					
				335					340					345					
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His					
				350					355					360					
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp					
				365					370					375					
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln					

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Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile					
				395					400					405					
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly					
				410					415					420					
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
				425					430					435					
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
				440					445					450					
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
				470					475					480					
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
				485					490					495					
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
				500					505					510					
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe					
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Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
				530					535					540					
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu					
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His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly					
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Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu					
				575					580					585					
Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp					
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Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln					
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Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu					
				635					640					645					
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val					
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Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val					

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680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
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785	790	795
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<210> 170

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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 agccatgact acgacgtggc gctgctgcag ctgcaccacc cgggtggtgcg 850  
 ctgggccgcc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900  
 agcccggcct gcactgctgg attacgggct ggggcgcctt gcgcgagggc 950  
 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000  
 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgctgt 1050  
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 ggtcagctgg ggccctgggt gtggccggcc taactacttc ggcgtctaca 1200  
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc cactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA



<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 175

aggcaggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50

ccaccgcccg ggctccgtgc cgccaagttt tcattttcca cttctctctg 100

ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150

gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200

ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctggt 250

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 tgcagtttca acatgacagc taaaaccttt ttcattcattc acggatggac 500  
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 gccaccagc tttacacgga tgcggtcaat aataccaggg tgggtgggaca 650  
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 aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

cggacgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50

cgagccacct cttccctcc cccgcttccc tgtegcgctc cgctggctgg 100  
acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150  
cggcaaagtt tggcccgaag aggaagtggc ctcaaaccac ggaggtggc 200  
gaccaggcca gaccaggggc gctcgctgcc tgcggggcgg ctgtaggcga 250  
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caccaggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500  
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 ctcacaaaaa gagtgcacaa aatgcttcta ttccatagct acggcattgc 3200  
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

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Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30	
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45	
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60	
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75	
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90	
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105	
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120	
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135	
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150	
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165	
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180	
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr				

185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200										210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					



470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro Ser	
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu Asp	
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn Leu	
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly Gly	
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg Arg	
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr Asn	
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro Ser	
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala Arg	
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro Pro	
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro Ala	
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu Pro	
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val	Val Gln Ala Leu Arg Gly	
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser Pro	
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp Asp	
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro	Gly Val Trp Val Ala Glu	
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 186  
agaacatagg agcagtcocca ctc 23

<210> 187  
<211> 23  
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<220>  
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<400> 187  
tgcctgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 188  
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
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gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
 aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
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 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
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<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe	1	5	10	15
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Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr	35	40	45	
Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile	50	55	60	
Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe	65	70	75	
Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe	80	85	90	
Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr	95	100	105	
Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys	110	115	120	
Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn	125	130	135	

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150

Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

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ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catcgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggc aacaacagta ttcattgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggc 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

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cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gtcctgcgc 150  
gccgccccgg agctggcccc cgcgcccttc acgtgcccc tccgggtggc 200  
cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccctg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgcctggcg 300  
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aatacttctt ttcttgtaaa cattgccact atttttgaat cagagaattt 650  
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aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
				20					25					30
Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45
Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	
				395					400					405	
Val	Ile	Gly	Ala	Thr	Val	Met	Glu	Gly	Phe	Tyr	Val	Ile	Phe	Asp	
				410					415					420	
Arg	Ala	Gln	Lys	Arg	Val	Gly	Phe	Ala	Ala	Ser	Pro	Cys	Ala	Glu	
				425					430					435	
Ile	Ala	Gly	Ala	Ala	Val	Ser	Glu	Ile	Ser	Gly	Pro	Phe	Ser	Thr	
				440					445					450	
Glu	Asp	Val	Ala	Ser	Asn	Cys	Val	Pro	Ala	Gln	Ser	Leu	Ser	Glu	
				455					460					465	
Pro	Ile	Leu	Trp	Ile	Val	Ser	Tyr	Ala	Leu	Met	Ser	Val	Cys	Gly	
				470					475					480	
Ala	Ile	Leu	Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Leu	Pro	Phe	Arg	
				485					490					495	
Cys	Gln	Arg	Arg	Pro	Arg	Asp	Pro	Glu	Val	Val	Asn	Asp	Glu	Ser	
				500					505					510	
Ser	Leu	Val	Arg	His	Arg	Trp	Lys								
				515											

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19



<210> 199  
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<223> Synthetic oligonucleotide probe  
  
<400> 199  
ggatgtagcc agcaactgtg 20  
  
<210> 200  
<211> 19  
<212> DNA  
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<400> 200  
gccttggtc gttctcttc 19  
  
<210> 201  
<211> 18  
<212> DNA  
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<223> Synthetic oligonucleotide probe  
  
<400> 201  
ggtcctgtgc ctggatgg 18  
  
<210> 202  
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<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 202  
gacaagacta cctccgttgg tc 22  
  
<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 203  
tgatgcacag ttcagcacct gttg 24  
  
<210> 204

<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA  
<213> Homo sapiens

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 taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30
Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45
Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60
Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	80	85	90
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	95	100	105
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	110	115	120
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	125	130	135
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	140	145	150
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150

caagcctcag gccagccacc tcccaccatc cgctgggttg tgaatgggca 200

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 ctgtgcccc aagctctggt gcctggcggg ccctgggacc gaaactctc 2100  
 agctcctcaa atgagctggt tactcgatcat ctccctccag caccctctt 2150  
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 caccacaggc tccctctcc atcctgctgc cagcagcccc catccccatc 2250  
 cttagcccct gcagtcccc tagccccag gcctcttccc tctctggccc 2300  
 cagcccagct tccagtgcgc tgtccagctc ctactgtca tccctggggg 2350  
 aggatcaaga cagcgtgctg acccctgagg aggtagccct gtgcttgaa 2400  
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<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20						25					30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
			35						40					45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
			50						55					60
Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
			65						70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
			80						85					90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
			95						100					105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
			110						115					120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
			125						130					135



Cys Gly Pro Pro	Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu	530	535	540
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp	545	550	555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser	560	565	570
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu	575	580	585
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp	590	595	600
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu	605	610	615
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln	620	625	630
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu	635	640	645
Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser	650	655	660
Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala	665	670	675
Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg	680	685	690
His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr	695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaaggacct acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgaccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 214  
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1869, 1887  
<223> unknown base

<400> 215  
ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50  
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gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150  
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200  
tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
agggcagggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

accctgtgga acctcacccct gcaagacgct ggggagtact ggtgtggggt 350  
 cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400  
 caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450  
 acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500  
 attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550  
 agacaggggc tgaggccct ccattgccag ggacttcca gtacgggcac 600  
 gaaaggactt ctctagtaac aggaacctct cctaccccag cgacctctcc 650  
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 aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750  
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 gtcagccgca ggctgatcg ccttctgcag ccacctgctc ctgtggagaa 850  
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 tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950  
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 tcccagggt ctctcttgc atgttccagc ctgacctaga agcgtttgct 1200  
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 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700  
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
			20					25					30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
			35					40					45	

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

50					55					60				
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met
				65					70					75
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu
				80					85					90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr
				95					100					105
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile
				110					115					120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser
				125					130					135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala
				140					145					150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu
				155					160					165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu
				170					175					180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr
				185					190					195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro
				200					205					210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala
				215					220					225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg
				230					235					240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu
				245					250					255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His
				260					265					270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln
				275					280					285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys
				290					295					300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro
				305					310					315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val
				320					325					330
Ser	Ala													

<210> 217  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 217  
ccctgcagtg cacctacagg gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtcttccc ctgcttggct gtgg 24

<210> 219  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
ggtgcaggaa gggtagggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtgtgaaa gaaccagtgg tctcgtcttg ttgccaggc tagagtgtac 150  
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
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ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgccca 400



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<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15
Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30
His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe				
				140					145					

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tggtggccct ggtc 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
gcaaggcaga ccagtcagc cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 224  
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccgggccggg cgcccgcggc ggcacatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctccgtgctc cgccgtgccc 250  
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tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgccgggtgga 650  
atgcaagtgc cacgggggtgt caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750  
gatggtgcc ctgagggtgga gccacgccgc gtgggtcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900  
ctgggcacga ggggcgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000  
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100  
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aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250  
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acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
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gctgtgcctt tgcagtcacg cccgagtcac ctttcacagc gctgttcctc 1900  
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<210> 226

<211> 351

<212> PRT

<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	1	5	10	15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	20	25	30	
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	35	40	45	
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	50	55	60	
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	65	70	75	
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	80	85	90	
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	95	100	105	
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	110	115	120	
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135	
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150	
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165	
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180	
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195	
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210	
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro				

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 227  
 gctgcagctg caaattccac tgg 23

<210> 228  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 228  
 tgggtgggaga ctgtttaaat tatcggcc 28

<210> 229  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctogtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

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gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctgggtacca cagtcctttg 200  
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gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350  
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
cgcgtgaccc agggccttggc tgaagccggc aggggccgtg aggacgtccg 500  
cactgagctg ttccggggcg tggaggccgt gaggtccag aacaactcct 550  
gcgagccgtg cccacgctcg tggctgtcct tcgagggtc ctgctacttt 600  
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650  
tgccagcgcg cacctgggtga tcgttggggg cctggatgag cagggttcc 700  
tcactcgga cagcgtggc cgtggttact ggctgggcct gagggtgtg 750  
cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
cagcttcagc cactggaacc agggagagcc caatgacgtc tgggggcgcg 850  
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000  
gctgtcacc tcctggctc ctggagctga ttgccaaaga gtttttttct 1050  
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tgtccagccc agtgccctggg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
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 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
 aaaaa 1355

<210> 231  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu  
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val  
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro  
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr  
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp  
275 280 285

Ile Cys Glu Lys Arg His Asn Cys  
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctgagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens



<400> 235

gccaggggaa gagggatgac cgacccgggg aaggtcgctg ggcagggcga 50  
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ctcccacgtc ctatctgcct ctgctggag gccaggccgt gcagcatcga 150  
agacaggagg aactggagcc tcattggccg gccggggcg ccggcctcgg 200  
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250  
cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgcgc 300  
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 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
1				5					10					15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val
				110					115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165

Asp	Ser	Leu	Asp	Leu	Cys	Asp	Gly	Asp	Arg	Trp	Arg	Glu	Gln	Ala	
				170					175					180	
Ala	Leu	Asp	Leu	Tyr	Pro	Tyr	Asp	Ala	Gly	Thr	Asp	Ser	Gly	Phe	
				185					190					195	
Thr	Phe	Ser	Ser	Pro	Asn	Phe	Ala	Thr	Ile	Pro	Gln	Asp	Thr	Val	
				200					205					210	
Thr	Glu	Ile	Thr	Ser	Ser	Ser	Pro	Ser	His	Pro	Ala	Asn	Ser	Phe	
				215					220					225	
Tyr	Tyr	Pro	Arg	Leu	Lys	Ala	Leu	Pro	Pro	Ile	Ala	Arg	Val	Thr	
				230					235					240	
Leu	Leu	Arg	Leu	Arg	Gln	Ser	Pro	Arg	Ala	Phe	Ile	Pro	Pro	Ala	
				245					250					255	
Pro	Val	Leu	Pro	Ser	Arg	Asp	Asn	Glu	Ile	Val	Asp	Ser	Ala	Ser	
				260					265					270	
Val	Pro	Glu	Thr	Pro	Leu	Asp	Cys	Glu	Val	Ser	Leu	Trp	Ser	Ser	
				275					280					285	
Trp	Gly	Leu	Cys	Gly	Gly	His	Cys	Gly	Arg	Leu	Gly	Thr	Lys	Ser	
				290					295					300	
Arg	Thr	Arg	Tyr	Val	Arg	Val	Gln	Pro	Ala	Asn	Asn	Gly	Ser	Pro	
				305					310					315	
Cys	Pro	Glu	Leu	Glu	Glu	Glu	Ala	Glu	Cys	Val	Pro	Asp	Asn	Cys	
				320					325					330	

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagcccccttc tctctctttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcaccgt gtctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagcccccttc tctctctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

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aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
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gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300  
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350  
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aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
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 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800  
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 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val
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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
				20					25					30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
				35					40					45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
				50					55					60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
				65					70					75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
				80					85					90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
				95					100					105
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala
				110					115					120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly
				125					130					135

Asp Thr Val Tyr	Asn Met Leu Arg Leu	Ser Glu Val Asp Ile	Asp
	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His	Lys Ile Lys Ser Cys	Glu
	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile	Ile Pro Arg Glu Ile	Lys
	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu	Glu Val Lys Lys Leu	Lys
	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu	Leu Ser Phe Gly Glu	Glu
	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn	Arg Val Ser Gln Ser	Met
	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp	Leu Leu Lys Asp Asp	Pro
	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu	Ser Glu Lys Gly Asp	Ala
	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp	Glu Ser Ala Glu His	Asp
	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn	Leu Met Arg Glu Arg	Ile
	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser	Ala Asn Val Lys Ser	Ala
	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser	Val Ser Arg Ser Glu	Glu
	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys	Arg Glu Leu Leu Ala	Ala
	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala	Lys Gln Ala Glu Lys	Arg
	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp	Gly Ala Val Ala Glu	Tyr
	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala	Leu Arg Lys Gln Gln	Ser
	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln	Thr Leu Ala Leu Leu	Asn
	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala	Ile Ala Glu Thr Pro	Glu
	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp	Met
	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Glu Arg Arg  
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<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcggagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatgggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250



<211> 24  
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<220>  
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ctggttcagc agtgaagg tctg 24

<210> 251  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
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gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253  
<211> 2456  
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<213> Homo sapiens

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gatgctgccc ggccgcctc ggctttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150  
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200  
gaccagcaca ggcggcgttt ttccttcgg aacgggaacg tctagcaacc 250  
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actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350  
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ccaagaggcc tcaagtggc accaaatatg gaaccctgca aggaaaacag 450  
atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500

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catgagccct gtggtggatg gtgtggtgat ccagatgac cctttggtgc 1450  
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<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

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Thr	Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe	20	25	30	
Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly	35	40	45	
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser	50	55	60	
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly	65	70	75	
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg	80	85	90	
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met	95	100	105	
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe	110	115	120	
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro	125	130	135	

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala	290	295	300
Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp	305	310	315
Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser	320	325	330
Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile	350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp	410	415	420

Ser Met Ser Pro	Val Val Asp Gly Val	Val Ile Pro Asp Asp Pro
425		430 435
Leu Val Leu Leu	Thr Gln Gly Lys Val	Ser Ser Val Pro Tyr Leu
440		445 450
Leu Gly Val Asn	Asn Leu Glu Phe Asn	Trp Leu Leu Pro Tyr Asn
455		460 465
Ile Thr Lys Glu	Gln Val Pro Leu Val	Val Glu Glu Tyr Leu Asp
470		475 480
Asn Val Asn Glu	His Asp Trp Lys Met	Leu Arg Asn Arg Met Met
485		490 495
Asp Ile Val Gln	Asp Ala Thr Phe Val	Tyr Ala Thr Leu Gln Thr
500		505 510
Ala His Tyr His	Arg Glu Thr Pro Met	Met Gly Ile Cys Pro Ala
515		520 525
Gly His Ala Thr	Thr Arg Met Lys Ser	Thr Cys Ser Trp Ile Leu
530		535 540
Pro Gln Glu Trp	Ala	
545		

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

agggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacgggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcattctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250

aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350

cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400

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ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcttgga 950

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gcctgggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050

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tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln
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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225



Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg  
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu  
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgccca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	
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Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	
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His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
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Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
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Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
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Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
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Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
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Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
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Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
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Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
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Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	

Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser	
				290					295					300	
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile	
				305					310					315	
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr	
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Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu	
				335					340					345	
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln	
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Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr	
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Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly	
				380					385					390	
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg	
				395					400					405	
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly	
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Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp	
				425					430					435	
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln	
				440					445					450	
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp	
				455					460					465	
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu	
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				485					490					495	
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser	
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Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln	
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Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu	
				530					535					540	
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn	
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Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val	
				560					565					570	

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	
				575					580					585	
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	
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Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	
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Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	
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Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	
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Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
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Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
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Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
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Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
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<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200  
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<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

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<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

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gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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cccgccctaa cttcctccgc ggggcccagc caccttcggg agtcggggtt 150



gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200  
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
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Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
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Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
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Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
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Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
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<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatgggtgtg tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350  
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450  
 gaccctatga cccagtcaa tgccaggtag gaatttggtc aggctctctt 500  
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<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

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 cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150  
 acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcttgctg 200  
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 ctcttgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350  
 tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
 gggggcgcca tatttcttct tgcaggtctg gctatttttag ttgccacagc 450  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

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gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtgggtg 250  
gcacccctcct gggagtata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgagg tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtag aatttggtca ggctctcttc actggctggg 500  
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<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctcccct cctggatgga tgcgccacc gtcacattgc cttccccan 50  
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300  
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgtt 350  
caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnnnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450

tcaggtctctc ttcaactgggt gggctgctgc ttctctctgc cttctgggag 500

gtgcctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50

gcagcacatt ncaagcaacc ccttgccctg aagggtggtg ncatcccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300

tgccaggtag gaatttggtc aggtctctct cactggctgg gctgctgctt 350

ctctctgcct tctgggaggt gccctacttt gctgttctctg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

agcaatgccc tgccccaggt ggaggattaa ttctatgnt ggggacaaca 50

ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatgggtggtt ggcattcttc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatattt cttnttgcat gtctggctat tttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50

cacagcatgg tatggcaata gaatcggtca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttgggc aggcctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacncctat gctggcgaac aacatntga ccgccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtga 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaacctg 200

ccttgatggt ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtga tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgaga tatttcttct tgcaggctctg 350

gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgettctctc tgccttctgg gaggtgccct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttgggc ttcattctgc ttcctgggat ggaatcggcg 50  
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgt gacnccccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200  
aatctgagca gcacattgca agcaaccntg ccttgatggt ggttggcatc 250  
ctcctgggag tgaatgcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcctg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350  
ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400  
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
tcaatgccag gtacgaattt ggtcaggctc tcttcaactg ctgggctgct 500  
gcttctctct gccttctggg aggtgcccta ctttgcgtgt cctgcgaa 548

<210> 280  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
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<210> 281  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 281  
gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
<211> 43



<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctcgcttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

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ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
tagaggaccc ccgcccgtgc cccgaccggg cccgccttt ttgtaaaact 150  
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200  
ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300  
ccgatgttgt caccaccaac ctaaagcttg gcaaccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcatc aaagacagaa acaccaatag tgtctaagtc 700  
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gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
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aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattggtg 1000  
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aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200  
ctttattaat gacaagggaa accatgagta atgccacaat ggcatattgt 1250  
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctcttaaaa tgacaccctt cctcgcctgt tgggtgctggc ccttggggag 1350  
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acgtggccca ctcccggccc aggctgcttt ccgtgtcttc agttctgtcc 1450  
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ctctggagag tctggtcagt tggaggtggg gtttattggg atgctggaga 1850  
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gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950  
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000  
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gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtac tagttgagag ttgactgtg aattaatttt 2200  
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250  
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly	Pro Phe Thr Asp Val	Val Thr Thr Asn Leu	
20		25	30
Lys Leu Gly Asn Pro	Thr Asp Arg Asn Val	Cys Phe Lys Val Lys	
35		40	45
Thr Thr Ala Pro Arg	Arg Tyr Cys Val Arg	Pro Asn Ser Gly Ile	
50		55	60
Ile Asp Ala Gly Ala	Ser Ile Asn Val Ser	Val Met Leu Gln Pro	
65		70	75
Phe Asp Tyr Asp Pro	Asn Glu Lys Ser Lys	His Lys Phe Met Val	
80		85	90
Gln Ser Met Phe Ala	Pro Thr Asp Thr Ser	Asp Met Glu Ala Val	
95		100	105
Trp Lys Glu Ala Lys	Pro Glu Asp Leu Met	Asp Ser Lys Leu Arg	
110		115	120
Cys Val Phe Glu Leu	Pro Ala Glu Asn Asp	Lys Pro His Asp Val	
125		130	135
Glu Ile Asn Lys Ile	Ile Ser Thr Thr Ala	Ser Lys Thr Glu Thr	
140		145	150
Pro Ile Val Ser Lys	Ser Leu Ser Ser Ser	Leu Asp Asp Thr Glu	
155		160	165
Val Lys Lys Val Met	Glu Glu Cys Lys Arg	Leu Gln Gly Glu Val	
170		175	180
Gln Arg Leu Arg Glu	Glu Asn Lys Gln Phe	Lys Glu Glu Asp Gly	
185		190	195
Leu Arg Met Arg Lys	Thr Val Gln Ser Asn	Ser Pro Ile Ser Ala	
200		205	210
Leu Ala Pro Thr Gly	Lys Glu Glu Gly Leu	Ser Thr Arg Leu Leu	
215		220	225
Ala Leu Val Val Leu	Phe Phe Ile Val Gly	Val Ile Ile Gly Lys	
230		235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100  
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200  
cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50  
gattacctcc ttaaatgaca cnttcctcg cctggttggtg ctggccnttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgtttt 350  
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcattctatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 287  
ccctggtggt tttgttcttt aattcggttg tgtaattntt gggaagattg 50  
ctttagtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
catatccatg ggatttaaata ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
<223> unknown base

<400> 288  
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gcaactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
actgattgac ccagcgcctt ggaaataaat ggcagtgcct tgttcantta 200  
aagggaccaa gctaaatttg tattgggttca tgtagtgaag tcaaactgtt 250  
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttggttg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggcatgtg gaggtggg 428

<210> 289  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 289  
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tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150  
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
atttaactta tttaatgtat ttcatctcat gttttcttat tgtcacaaga 300  
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
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ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200  
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccg 250  
cccaggctgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400  
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
atgcatatth aanttattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtac agttaatgct gcgtgctgct gaantctggt ggggtgaantg 600  
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagcccaaag gaattgcaact gtggcagcat cagacgtact cgtcataagt 200  
gagaggcgtg tggtgactga ttgaccagc gctttggaaa taaatggcag 250  
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tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450  
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<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150  
gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200  
tgcagccttg acctcctggg ttcaagcga cctgctgagt agctgggact 250  
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300  
atTTTTcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350  
atTTTatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400  
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aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650  
gcaccgacag cagggtcagc atcttgga caaaggttctt aaccaatttc 700  
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750  
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agctagtggg ggtgaccaa gagagggtac cagagagcat ctgcaggaga 950  
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 ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700  
 gtgggcactt caatgccaaag tatatactct tctttacatg gtgatgagtt 1750  
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 accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850  
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 aatgtgaaat tgcataagata aaggtagatg gtaaagcaat tagtatcaga 1950  
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 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150  
 caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200  
 cctagtttag aaatagggaa gctgagacat ttaagatct caagttttta 2250  
 tttactaat actcaaaata tggacttttc atgtatgcat aggggaagaca 2300  
 cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400  
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450  
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<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20					25					30				
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu
				35					40					45
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr
				50					55					60
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu
				65					70					75
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn
				80					85					90
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu
				95					100					105
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg
				110					115					120
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp
				125					130					135
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu
				140					145					150
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu
				155					160					165
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly
				170					175					180
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser
				185					190					195
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala
				200					205					210
Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu
				215					220					225
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln
				230					235					240
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys
				245					250					255
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp
				260					265					270
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala
				275					280					285
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys
				290					295					300
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggagggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

<400> 300

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tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gcccattggag tgaatgctca cgcacctgcg ggggaggggc ctccactact 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aacccatgtt cactcaagtg 500  
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550  
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tgccaaattg ttggtgcga tcaccagctg ggaagcaccg tcaaggaaga 650  
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gaccttgctc cagccagtga cggatacaag cagatcatgc cttatgacct 1250  
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 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800  
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 ttagtttcaa aaaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

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ctgggcgggg cgctgtggtt ggcggcccgc cgttcgtgg ggcccagggt 150
ccagcggctg cgcagaggcg gggaccccgc cctcatgcac gggaagactg 200
tgctgatcac cggggcgaaac agcggcctgg gccgcgccac ggccgcccag 250
ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
cgccgaggag gcggcgggct agctccgccg cgagctccgc caggccgcgcg 350
agtgcggccc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
gagctggacc tcgcctcgct gcgctcgggt gcgccttct gccaggaaat 450
gctccaggaa gaggctaggc tggatgtctt gatcaataac gcagggatct 500
tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
caaaagtcca gctccagca ggattgtggt agtttcttcc aaactttata 650
aatacggaga catcaatctt gatgactga acagtgaaca aagctataat 700
aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

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ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800  
 atcctgggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900  
 agtagaaggt gccagactt ccatttattt ggcctcttca cctgaggttag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatgggtt ggcctgctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatgggtg tggattgaga 1150  
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 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400  
 agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttgggaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly	1	5	10	15
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln	20	25	30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr	35	40	45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly				



95					100					105				
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg
				110					115					120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg
				125					130					135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr
				140					145					150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His
				155					160					165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys
				170					175					180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr
				185					190					195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser
				200					205					210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile
				215					220					225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val
				230					235					240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly
				245					250					255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu
				260					265					270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr
				275					280					285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly
				290					295					300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala
				305					310					315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val
				320					325					330
Met	Val	Gly	Leu	Leu	Lys									
				335										

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagtt 250  
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300  
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
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tggaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

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ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150  
cttcttatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200  
gggtttttac tctgttaaca actgaaataa caagtcttgc tacagagaat 250  
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tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
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caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
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cggacaacta tagagttttt gaacgagtag cgaatatattt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataattctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850  
gataaatgtg ttctctttgt ccgagaaata acatttgaaa atggagagga 900  
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gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
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 gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
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 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

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Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	
				20					25					30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	
				35					40					45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	
				50					55					60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	
				65					70					75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	
				80					85					90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	
				95					100					105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	
				110					115					120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	
				125					130					135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	
				140					145					150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	
				155					160					165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	
				170					175					180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	
				185					190					195	

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 48  
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccctttccta acccaacca acctagccn gtcccagccg 150  
ccagcgctg tccctgtcnc ggancccagc gtnaccatgc atcctgccgt 200  
cttcctatcc ttaccogacc tcagatgctc cttctgtctc ctggttaactt 250  
gggtttttac tctgttaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaacna tgctgatgtg gcttttagtca atttttatgc 350  
tgactggtgt cgtttcagtc agatgtggca tccaatttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttecta tccttaccog acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgog ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa gtttccacat 600



ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcatatgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcatctgtc atgtcgtatga ttatatatgg 950  
 atacattttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt ctttaagcata agtaaacatg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactctg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaatata ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10				15	
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25				30	
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40				45	
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55				60	
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70				75	
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85				90	
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100				105	

Ile	Met	Asn	Ala	Asp	Ile	Leu	Ala	Tyr	Cys	Gln	Lys	Glu	Gly	Trp
				110					115					120
Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ala	Phe	Phe	Tyr	Tyr	Leu	Tyr
				125					130					135
Gly	Met	Ile	Tyr	Val	Leu	Val	Ser	Ser						
														140

<210> 323  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
 tgtaataccc tgaatcccct tgtactccca gagtacctca tccacgcttt 100  
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150  
 atatgccctt cttggcatat catatttgga ggtatatgag tagaccagtg 200  
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
 tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300  
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
 tagaacaaca cacagaagaa ttggtccagt taagtgcatt caaaaagcca 400  
 ccaaataaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
 gaatctgac agttacttta aaaaatg 477

<210> 324  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 324  
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 325  
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tggcgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggaccaact ggggtccccg ccgtgtgtgc tgctgacct ggccttgcc 150  
ggaggttcgg ggaccgcttc ggctgaagca ttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagagggtg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500  
 aactctgggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
 gttatatcc agtctaagcc agaaatccag tacgcaccac atttggagca 650  
 ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
 aactcttgtc ctctcgggtga tggatttgct ttggatttgt tgtgcaactg 850  
 ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900  
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050  
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100  
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
 caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10					15
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100					105

Gln Ser Asp Glu Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn Gln
110	115 120
Leu Pro Phe Ala Glu Leu Arg Gln Glu	Gln Leu Met Ser Leu Met
125	130 135
Pro Lys Met His Leu Leu Phe Pro Leu	Thr Leu Val Arg Ser Phe
140	145 150
Trp Ser Asp Met Met Asp Ser Ala Gln	Ser Phe Ile Thr Ser Ser
155	160 165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp	Gly Lys Ile Val Ile Phe
170	175 180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala	Pro His Leu Glu Gln Glu
185	190 195
Pro Thr Asn Leu Arg Glu Ser Ser Leu	Ser Lys Met Ser Tyr Leu
200	205 210
Gln Met Arg Asn Ser Gln Ala His Arg	Asn Phe Leu Glu Asp Gly
215	220 225
Glu Ser Asp Gly Phe Leu Arg Cys Leu	Ser Leu Asn Ser Gly Trp
230	235 240
Ile Leu Thr Thr Thr Leu Val Leu Ser	Val Met Val Leu Leu Trp
245	250 255
Ile Cys Cys Ala Thr Val Ala Thr Ala	Val Glu Gln Tyr Val Pro
260	265 270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp	Leu Glu Phe Met Asn Glu
275	280 285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser	Ser Leu Val Val Val Arg
290	295 300
Ser Lys Thr Glu Asp His Glu Glu Ala	Gly Pro Leu Pro Thr Lys
305	310 315
Val Asn Leu Ala His Ser Glu Ile	
320	

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgcag agagggttga 100

ggctgttttc aatttgcag tttgtggatg atggaattga cttaaatacga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttctcttaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

cacactggcc ggatctttta gagtcctttg accttgacca agggtcngga 50  
aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100  
cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150  
tgctgaccat ggccttgccc ggaggttcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagagggtg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350  
gacttaaatic gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
atgcacctac tctttcctct aactctggtg aggtcattct ggagtacat 550  
gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cgggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcattctg 100  
agggcgcacg gcccgcgacc gagcgtgagg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggttgggga ttcttgtttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaacctt tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgag agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggett c tgggtcaaggg 850  
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtat ttt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200  
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgttttaaa tgcgtctgt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500  
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagt gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacttt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
1				5					10				15	

Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25					30	



Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp	35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg	50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg	65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50

ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100

nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150

ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200

caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250

attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300

tccaagaagg ctaagaact tgtatcttct ctacttaata gaactaaggg 350

ctttatccaa agtggttacca ttcttngagc gcccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
acttcatgaa atcaagtcatt ttcttttgca ttttgatgag aattcatttt 500  
tttgctg 507

<210> 339  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac tttcgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggacttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttgat acagtgtctt acaacatgtt ggggggtggac agcgtatgat 300

gctggtgggc gcccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggccaca atgcccctg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agaggggtggt ggcagtgtct ctgaagggtcc ataaaagaaa 550

aaagagaagt gtggttaaggg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggatgcttc 800

attccagcct caggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatectcatt 950  
gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050  
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150  
gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200  
ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

Met	Glu	Leu	Pro	Phe	Val	Thr	His	Leu	Phe	Leu	Pro	Leu	Val	Phe
1				5					10					15
Leu	Thr	Gly	Leu	Cys	Ser	Pro	Phe	Asn	Leu	Asp	Glu	His	His	Pro
				20					25					30
Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val
				35					40					45
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala
				50					55					60
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg
				65					70					75
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His
				80					85					90
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn
				95					100					105
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly
				110					115					120

Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 22  
<223> unknown base

<400> 347  
cacagtcccc caccatcact cntcccatc ottccaactt tatttttagc 50  
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150  
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttcct 200  
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300  
gggggtggac agcgatggat gctgggtggc gccccctggg atgggccttc 350  
aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400  
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
tggtgatgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 348  
agggacagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttcacagcag gatg 24

<210> 350  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 350  
ggaactcccc ttgcgtcactc acctgttctt gcccctggtg ttcct 45

<210> 351  
<211> 2056  
<212> DNA  
<213> Homo sapiens

<400> 351  
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450  
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
ccccagcagc tgggtgctcac tcaactgaagg tcctgagtgt gatgtcactg 550  
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750  
gcctactgga ggaggagacc tggtgccgag gaacatgtca aaatggtgag 800  
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950  
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cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050  
 gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100  
 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
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 gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350  
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 cggtcctaag ttttctcctc tgtaatgggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550  
 tacaccagc acttgcaagg ctagaggga actggtgaca ctctacagtc 1600  
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 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgtccttt tttctgttg taaagtacag 2000  
 aattcagcaa ataaaaagg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1					5					10				15

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
				20					25					30



Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
tcctgctgat gcacatctgg gtttggaaca aggaggttgc ttcgagccgc 50  
cctttctagc ttctggccg gctctagaac aattcaggct tcgctgacgac 100  
tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcttt attttggaac gaaacaatgt tctaggtcaa actgagtcta 200  
ccaaatgcag actttcaca tggttctaga agaaatctgg acaagtcttt 250  
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450  
tggatcccca gcagctgggt ctcactcact gaaggtcctg agtgtgatgt 500  
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600  
agaaactcaa ccacacctac ccgacctggg atggagatca ccaaagatgg 650  
cttncaacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
gaaccocctt cgcccgctgg ggtatctctc gagaaaagag aggcccaata 800  
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
ggcgctgggt tgat 864

<210> 354  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 354  
aggcttcgct gcgactagac ctc 23

<210> 355  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 355  
ccaggtcggg taaggatggt tgag 24

<210> 356  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
cccacgcgtc cgcccacgcg tccgaggac aagagagaag agagactgaa 50  
acaggagagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200  
tgagagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250  
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300  
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350  
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400  
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450  
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500  
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ataatctcca gggaaacttc gtgccagggc ctcctttctg gggcctggtg 750  
 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800  
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 tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900  
 catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950  
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 cgctgcctcc cgcgggccca atggcctggc cattctcagc ctctttgtca 1150  
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 gagcctggag ctctgtttcc ctgaatcctt cggcttcac acctatcagg 1300  
 gctctctcag caccgcccc tgctccgaga ctgtcacctg gatcctcatt 1350  
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 gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
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 cggcaccgag agaggcgctg ccgaggcccc aactaccgcc tgcattgtga 1550  
 tgggtgtcccc catggtcgct gagactcccc ttcgaggatt gcaccgccc 1600  
 gtctaagcc tcccacaag gcgaggggag ttaccocctaa aacaaagcta 1650  
 ttaaagggac agaatactta 1670

<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
				20					25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
				50					55					60

Leu	Cys	Ala	Val	Gly	Lys	Arg	Gln	Ser	Pro	Val	Asp	Val	Glu	Leu	65	70	75
Lys	Arg	Val	Leu	Tyr	Asp	Pro	Phe	Leu	Pro	Pro	Leu	Arg	Leu	Ser	80	85	90
Thr	Gly	Gly	Glu	Lys	Leu	Arg	Gly	Thr	Leu	Tyr	Asn	Thr	Gly	Arg	95	100	105
His	Val	Ser	Phe	Leu	Pro	Ala	Pro	Arg	Pro	Val	Val	Asn	Val	Ser	110	115	120
Gly	Gly	Pro	Leu	Leu	Tyr	Ser	His	Arg	Leu	Ser	Glu	Leu	Arg	Leu	125	130	135
Leu	Phe	Gly	Ala	Arg	Asp	Gly	Ala	Gly	Ser	Glu	His	Gln	Ile	Asn	140	145	150
His	Gln	Gly	Phe	Ser	Ala	Glu	Val	Gln	Leu	Ile	His	Phe	Asn	Gln	155	160	165
Glu	Leu	Tyr	Gly	Asn	Phe	Ser	Ala	Ala	Ser	Arg	Gly	Pro	Asn	Gly	170	175	180
Leu	Ala	Ile	Leu	Ser	Leu	Phe	Val	Asn	Val	Ala	Ser	Thr	Ser	Asn	185	190	195
Pro	Phe	Leu	Ser	Arg	Leu	Leu	Asn	Arg	Asp	Thr	Ile	Thr	Arg	Ile	200	205	210
Ser	Tyr	Lys	Asn	Asp	Ala	Tyr	Phe	Leu	Gln	Asp	Leu	Ser	Leu	Glu	215	220	225
Leu	Leu	Phe	Pro	Glu	Ser	Phe	Gly	Phe	Ile	Thr	Tyr	Gln	Gly	Ser	230	235	240
Leu	Ser	Thr	Pro	Pro	Cys	Ser	Glu	Thr	Val	Thr	Trp	Ile	Leu	Ile	245	250	255
Asp	Arg	Ala	Leu	Asn	Ile	Thr	Ser	Leu	Gln	Met	His	Ser	Leu	Arg	260	265	270
Leu	Leu	Ser	Gln	Asn	Pro	Pro	Ser	Gln	Ile	Phe	Gln	Ser	Leu	Ser	275	280	285
Gly	Asn	Ser	Arg	Pro	Leu	Gln	Pro	Leu	Ala	His	Arg	Ala	Leu	Arg	290	295	300
Gly	Asn	Arg	Asp	Pro	Arg	His	Pro	Glu	Arg	Arg	Cys	Arg	Gly	Pro	305	310	315
Asn	Tyr	Arg	Leu	His	Val	Asp	Gly	Val	Pro	His	Gly	Arg			320	325	

<210> 359

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 359  
tctgctgagg tgcagctcat tcac 24

<210> 360  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 360  
gaggctctgg aagatctgag atgg 24

<210> 361  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038  
<212> DNA  
<213> Homo sapiens

<400> 362  
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gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150  
gcagctccct tcccacccca actgcaggtc taattttgga cgttttgcct 200  
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250  
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gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350  
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	



Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu		35	40	45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn		50	55	60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln		65	70	75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val		80	85	90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp		95	100	105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu		110	115	120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln		125	130	135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His		140	145	150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys		155	160	165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly		170	175	180
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile		185	190	195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly		200	205	210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser		215	220	225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys		230	235	240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu		245	250	255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His		260	265	270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser		275	280	285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg		290	295	300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala		305	310	315

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
500	

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag cccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 369  
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50  
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100  
agagaaagcc gagcagagct ggggtggcgtc tccgggcccgc cgctccgacg 150  
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gcatgaggct cctggcggcc gcgctgctcc tgctgctget ggcgctgtac 250  
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gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatgggt atcatcacca ccaagagcgt gtccagggtac 400  
 cgagggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450  
 catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500  
 aggggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550  
 gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600  
 aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650  
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 gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750  
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 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370  
 <211> 111  
 <212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu	
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20					25					30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys	
				35					40					45	
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	
				50					55					60	
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val	
				65					70					75	
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	
				80					85					90	
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	
				95					100					105	
Arg	Arg	Val	Tyr	Glu	Glu										
				110											

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

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tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

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 gacacttctg aaactcagcc aaggacactt gatatttttt aattacaatg 2900  
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 tgaagaaaga gtcaatgaga ttttgcccag cacatggagc tgtaatccag 3000  
 agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050  
 aatctgtacg gttctgtgca aagaggtggt ttgccagcct gaactatatt 3100  
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<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150



Ser Asn Asp Arg Gly Glu Asp Glu Asp	Ile His Asp Gln Asn Ser
155	160 165
Lys Lys Pro Val Met Val Tyr Ile His	Gly Gly Ser Tyr Met Glu
170	175 180
Gly Thr Gly Asn Met Ile Asp Gly Ser	Ile Leu Ala Ser Tyr Gly
185	190 195
Asn Val Ile Val Ile Thr Ile Asn Tyr	Arg Leu Gly Ile Leu Gly
200	205 210
Phe Leu Ser Thr Gly Asp Gln Ala Ala	Lys Gly Asn Tyr Gly Leu
215	220 225
Leu Asp Gln Ile Gln Ala Leu Arg Trp	Ile Glu Glu Asn Val Gly
230	235 240
Ala Phe Gly Gly Asp Pro Lys Arg Val	Thr Ile Phe Gly Ser Gly
245	250 255
Ala Gly Ala Ser Cys Val Ser Leu Leu	Thr Leu Ser His Tyr Ser
260	265 270
Glu Gly Leu Phe Gln Lys Ala Ile Ile	Gln Ser Gly Thr Ala Leu
275	280 285
Ser Ser Trp Ala Val Asn Tyr Gln Pro	Ala Lys Tyr Thr Arg Ile
290	295 300
Leu Ala Asp Lys Val Gly Cys Asn Met	Leu Asp Thr Thr Asp Met
305	310 315
Val Glu Cys Leu Arg Asn Lys Asn Tyr	Lys Glu Leu Ile Gln Gln
320	325 330
Thr Ile Thr Pro Ala Thr Tyr His Ile	Ala Phe Gly Pro Val Ile
335	340 345
Asp Gly Asp Val Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln
350	355 360
Gly Glu Phe Leu Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly
365	370 375
Glu Gly Leu Lys Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly
380	385 390
Val Thr Pro Asn Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp
395	400 405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr
410	415 420
Ile Lys Phe Met Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu
425	430 435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
				800					805					810
His	Ser	Thr	Thr	Arg	Val									
				815										

<210> 376  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 376  
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 377  
 aacccccgag ccaaaagatg gtcac 25

<210> 378  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 378  
 gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379  
 <211> 2461  
 <212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50  
ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ctttcttctt 100  
ttgttggggc ctgggcaggg gccacagcaa gtcggggcgg gtcaaactgt 150  
cgagtacttg aaacgggagc actcgtctgc gaagccctac cagggtgtgg 200  
gcacaggcag ttctcactg tggaatctga tgggcaatgc catggtgatg 250  
accagttata tccgccttac cccagatatg caaagtaaac aggggtgcctt 300  
gtggaaccgg gtgccatgtt tcttgagaga ctgggagttg cagggtgcact 350  
tcaaaatcca tggacaagga aagaagaatc tgcattggga tggcttggca 400  
atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450  
ggacaaatth gtggggctgg gaggatthgt agacacctac cccaatgagg 500  
agaagcagca agagcgggta tccccctaca tctcagccat ggtgaacaac 550  
ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600  
aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttctggtga 650  
ttcgtactgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700  
catgagtggg gggactgcat tgaagtggcc ggagtcggcc tgccccgcgg 750  
ctactacttc ggcacctcct ccatcactgg ggatctctca gataatcatg 800  
atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850  
gaggaaaagc tccatcgaga tgtgttcttg cctcagtggt acaatatgaa 900  
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tctcatcgt ctttttctcc ctggtgtttt ctgtatttgc catagtcatt 1000  
ggatcatatc tctacaacaa atggcaggaa cagagccgaa agcgcttcta 1050  
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gaaggagcag gcactggcct gagcatgcag cctggagagt gttcttgtct 1150  
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gaccccgcat tcccatggtt gtgcatgggg acatctaact ctggtctggg 1250  
aagccacca cccagggca atgctgtgt gatgtgcctt tccctgcagt 1300  
ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350

caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400  
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450  
 taacaccaca ggctttctga ccatccattc gttgggtttt gcatttgacc 1500  
 caaccctctg cctacctgag gagctttctt tggaaaccag gatggaaact 1550  
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 caaaagcaac atttgcattg tggctctgacc atgtggagat gtttctggac 1950  
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 ggccgcatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met	Ala	Ala	Thr	Leu	Gly	Pro	Leu	Gly	Ser	Trp	Gln	Gln	Trp	Arg
1				5				10					15	

Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
			20					25					30	

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly				35	40	45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro				50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met				65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp				80	85	90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe				95	100	105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln				110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr				125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys				140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu				155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn				170	175	180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr				185	190	195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp				200	205	210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met				215	220	225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val				230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser				245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys				260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu				275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro				290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe				305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys  
335 340 345

Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ccttggtcg tggcagcagt gg 22

<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

cactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaactgt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

ccgagccggg cgcgcagcga cggagctggg gccgcctgg gaccatgggc 50

gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100

ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150

tggggctctgg ctcaagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250  
ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300  
tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350  
cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400  
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cagaccccg tttatgaagct cttttgtact gcaacatccc cagtgtggcc 500  
gagcgcagca tggaaggtca tgcccgcat cattttaagc tgggtctcagt 550  
gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600  
aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650  
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agcctctttc gaaagccct tgaactcctt gcctctttac ccaaaccacc 750  
cattgtgtga gatgggagag ctacacaga caggagtgtg gcagcatttg 800  
cagaacggtc agctgctgag ggatatctat ctaaagaaac acaaactcct 850  
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met	Leu	Phe	Arg	Asn	Arg	Phe	Leu	Leu	Leu	Leu	Ala	Leu	Ala	Ala
1				5					10					15
Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25					30
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40					45
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55					60
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
				185					190					195
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210
Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser	Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr	Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His	Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu	His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp	Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His	Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtggtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50

cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100

atcctttctg ggagttcaag attgtgcagt aattggtttag gactctgagc 150

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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

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Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570



Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
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Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

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cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150  
 ctggaagacc tcaccatggg acgccccga cctcgtgagg ccaagacgtg 200  
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	
				80					85					90	
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	
				95					100					105	
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	
				125					130					135	
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	
				140					145					150	
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	
				155					160					165	
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	
				170					175					180	
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	
				185					190					195	
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	
				200					205					210	
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	
				215					220					225	
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	
				230					235					240	
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	
				245					250					255	
Ile	Gly	Ser	Lys	Gly											
				260											

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggagg gctgagcgcc tectgaggcc cggcctgcgc 50

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gccccgccc gggccgcgc ccgcgcccgc gccaggtga gcgtccgcc 150

cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatcctccc ggcgggccgc gctgcgagcg ccccgccagt ccgcgcccgc 300

gccgccctcg cctgtgcgc cctgcgcgc ctgcgcaccc gcggcccag 350

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cccaaccct acgatgaaga gggcgtccgc tggagggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccagg 600

gcctgcgtat gctacaatga gcccaagggt acgacaagct gccccagca 650

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 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
				20					25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser	Glu Val
275		280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys	Arg
290		295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr	Gly Pro
305		310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu	Pro Leu
320		325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys	Ala Ser
335		340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala	Leu Lys
350		355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly	Ser Gly
365		370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro	Gly Ser
380		385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser	Glu Pro
395		400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly	Cys Ser
410		415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln	Ala Gly
425		430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly	Ala Leu
440		445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala	Leu Val
455		460	465
Leu Trp Thr Val	Leu Gly Pro Cys		
470			

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100

agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150

agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgaga 200

caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250

cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300

cctttgtcac caatttagca aaggacctgg gtctggagca gaggggaattc 350

tccaggcggg gggtaggggt tgtttccaga ggaacaaac tacatttgca 400

gctcaatcag gagaccgagg atttgttgct aaatgagaaa ttggaccgtg 450

aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500

ctagagagtc ccttcagatt ttttcaagct gagctgcaag taatagacat 550

aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600

cagagagcag tctcctggg actacgtttc ctctgaagaa tgccgaagac 650

ttagatgtag gccaaaacaa tattgagaac tatataatca gccccaactc 700

ctattttcgg gtctcaccg gcaaacgcag tgatggcagg aaatacccag 750

agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800

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 ggttcaatat tcagtacca tagttgactt ttacattcca taggtatttt 2600  
 atttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650  
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 tgttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu	1	5	10	15
Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu	20	25	30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe	35	40	45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe	50	55	60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His	65	70	75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys	80	85	90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu	95	100	105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala	110	115	120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu	125	130	135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly	140	145	150	

Thr Thr Phe Pro	Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala
440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser	
455	460	465
Pro Ala Leu His	Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser	
470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp	
485	490	495
Pro His Leu Pro	Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn	
500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln	
515	520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala	
530	535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val Val Val Leu Asp Ala Asn	
545	550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala	
560	565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu	
575	580	585
Val Thr Lys Val	Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala	
590	595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe	
605	610	615
Gly Val Trp Ala	His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu	
620	625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg Leu Val Val Leu Val Lys	
635	640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val	
650	655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu	
665	670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu	
680	685	690
Val Val Ala Leu	Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val	
695	700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala	
710	715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe  
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgtca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50  
 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100  
 cggtcgacga ccgccccgcg tcatgcggct cctcggtggg tggcaagtat 150  
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
 agtggtcgct tatggtcaga ggagcagcct gctcacctc tccaggtggg 250  
 ggctgtgtac ctgggtgagg aggagctcct gcatgaccg atgggccagg 300  
 acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350  
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500  
 cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
 atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600  
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650  
 actctgaaaa ttttaaatat gtcacaggac cttatggatt ttctgaacc 700  
 aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggtgccgct 750  
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 gctcttcaact ttttggcact ggatgcatct cagcacagca gcctttctac 850  
 caggtttggc accgtagctg ttcctaatat tttattattt caaggagcta 900  
 aaccaatggc cagatttaaat catacagatc gaacactgga aacactgaaa 950  
 atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000  
 aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagt 1050  
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 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350  
 caataagcaa atgcaaaaat attcaatag 1379

<211> 360

<212> PRT

<213> Homo sapiens

<400> 410

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Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val	
				20					25					30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	
				35					40					45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	
				50					55					60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	
				65					70					75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	
				80					85					90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	
				170					175					180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
				185					190					195	
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	
				200					205					210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
				215					220					225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
				230					235					240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	



	260		265		270
Ala Lys Pro Met	Ala Arg Phe Asn His	Thr Asp Arg Thr Leu Glu			
	275	280			285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln	Thr Gly Ile Glu Ala Lys			
	290	295			300
Lys Asn Val Val	Val Thr Gln Ala Asp	Gln Ile Gly Pro Leu Pro			
	305	310			315
Ser Thr Leu Ile	Lys Ser Val Asp Trp	Leu Leu Val Phe Ser Leu			
	320	325			330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr	Ala Thr Ile Arg Thr Glu			
	335	340			345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln	Glu Gln Glu His Val Glu			
	350	355			360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgg cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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agggccctgg ctgctgctg ctgctcttcc tcgcctcgca ctgctgcctg 100  
ggctcggcgc gggggtctt cctctttggc cagcccgact tctcctacaa 150  
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gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Phe Leu Ala Ser

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His Cys Cys Leu Gly	Ser Ala Arg Gly	Leu Phe Leu Phe Gly	Gln
20		25	30
Pro Asp Phe Ser Tyr	Lys Arg Ser Asn	Cys Lys Pro Ile Pro	Val
35		40	45
Asn Leu Gln Leu Cys	His Gly Ile Glu	Tyr Gln Asn Met Arg	Leu
50		55	60
Pro Asn Leu Leu Gly	His Glu Thr Met	Lys Glu Val Leu Glu	Gln
65		70	75
Ala Gly Ala Trp Ile	Pro Leu Val Met	Lys Gln Cys His Pro	Asp
80		85	90
Thr Lys Lys Phe Leu	Cys Ser Leu Phe	Ala Pro Val Cys Leu	Asp
95		100	105
Asp Leu Asp Glu Thr	Ile Gln Pro Cys	His Ser Leu Cys Val	Gln
110		115	120
Val Lys Asp Arg Cys	Ala Pro Val Met	Ser Ala Phe Gly Phe	Pro
125		130	135
Trp Pro Asp Met Leu	Glu Cys Asp Arg	Phe Pro Gln Asp Asn	Asp
140		145	150
Leu Cys Ile Pro Leu	Ala Ser Ser Asp	His Leu Leu Pro Ala	Thr
155		160	165
Glu Glu Ala Pro Lys	Val Cys Glu Ala	Cys Lys Asn Lys Asn	Asp
170		175	180
Asp Asp Asn Asp Ile	Met Glu Thr Leu	Cys Lys Asn Asp Phe	Ala
185		190	195
Leu Lys Ile Lys Val	Lys Glu Ile Thr	Tyr Ile Asn Arg Asp	Thr
200		205	210
Lys Ile Ile Leu Glu	Thr Lys Ser Lys	Thr Ile Tyr Lys Leu	Asn
215		220	225
Gly Val Ser Glu Arg	Asp Leu Lys Lys	Ser Val Leu Trp Leu	Lys
230		235	240
Asp Ser Leu Gln Cys	Thr Cys Glu Glu	Met Asn Asp Ile Asn	Ala
245		250	255
Pro Tyr Leu Val Met	Gly Gln Lys Gln	Gly Gly Glu Leu Val	Ile
260		265	270
Thr Ser Val Lys Arg	Trp Gln Lys Gly	Gln Arg Glu Phe Lys	Arg
275		280	285
Ile Ser Arg Ser Ile	Arg Lys Leu Gln	Cys	

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 416  
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<210> 417  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
cctcacaggt gcactgcaag ctgtc 25

<210> 418  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 418  
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<210> 419  
<211> 1830  
<212> DNA  
<213> Homo sapiens

<400> 419  
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cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150  
gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200  
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gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420  
 <211> 560  
 <212> PRT  
 <213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg	1	5	10	15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	20	25	30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	35	40	45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	50	55	60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	65	70	75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	80	85	90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	95	100	105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	110	115	120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	125	130	135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	140	145	150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	155	160	165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	170	175	180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	185	190	195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	200	205	210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	215	220	225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	230	235	240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	245	250	255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu	260	265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser Gly	275	280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu	290	295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu Ala	305	310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe	320	325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala	335	340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro Val	350	355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu Gly	365	370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile	380	385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser Glu	395	400	405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp	410	415	420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser	425	430	435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln	440	445	450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly	455	460	465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala	470	475	480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala Arg	485	490	495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His Pro	500	505	510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr	515	520	525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala	530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
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<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag ccctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cggttcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtccacatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50

ccatcatttg ctgaagtgga ccaactagtt cccagtagg ggtctctccc 100

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tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

aaggttggtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300



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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met Met Gln Leu Leu Gln Leu Leu Leu Gly Leu Leu Gly Pro Gly

1

5

10

15

Gly Tyr Leu Phe	Leu Leu Gly Asp Cys	Gln Glu Val Thr Thr	Leu
	20	25	30
Thr Val Lys Tyr	Gln Val Ser Glu Glu	Val Pro Ser Gly Thr	Val
	35	40	45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly	Arg Glu Glu Arg Arg	Arg
	50	55	60
Gln Ala Gly Ala	Ala Phe Gln Val Leu	Gln Leu Pro Gln Ala	Leu
	65	70	75
Pro Ile Gln Val	Asp Ser Glu Glu Gly	Leu Leu Ser Thr Gly	Arg
	80	85	90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg	Gln Trp Asp Pro Cys	Leu
	95	100	105
Val Ser Phe Asp	Val Leu Ala Thr Gly	Asp Leu Ala Leu Ile	His
	110	115	120
Val Glu Ile Gln	Val Leu Asp Ile Asn	Asp His Gln Pro Arg	Phe
	125	130	135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile	Ser Glu Ser Ala Ser	Leu
	140	145	150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala	Leu Asp Pro Asp Thr	Gly
	155	160	165
Pro Asn Thr Leu	His Thr Tyr Thr Leu	Ser Pro Ser Glu His	Phe
	170	175	180
Ala Leu Asp Val	Ile Val Gly Pro Asp	Glu Thr Lys His Ala	Glu
	185	190	195
Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305		315
Pro Ala Tyr Glu	Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn	
320		330
Pro Ile Pro Ala	His Cys Lys Val Leu Ile Lys Val Leu Asp Val	
335		345
Asn Asp Asn Ile	Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro	
350		360
Ser Leu Val Ser	Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu	
365		375
Val Met Ala Asp	Asp Leu Asp Ser Gly His Asn Gly Leu Val His	
380		390
Cys Trp Leu Ser	Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr	
395		405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg	
410		420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln	
425		435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile	
440		450
Ser Asp Ile Asn	Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr	
455		465
Glu Val Ser Thr	Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile	
470		480
Thr Ile Lys Ala	His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val	
485		495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val Ala His Leu Val Ala Ile	
500		510
Asp Ser Asn Thr	Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr	
515		525
Glu Glu Met Ala	Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser	
530		540
Gly Gln Pro Met	Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu	
545		555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu	
560		570
Ser Asp Gly Lys	Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr	
575		585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750
Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu  
1175 1180

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

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<213> Artificial Sequence

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<400> 428

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<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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ggcctcgggg agtggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctcca gatactatgt 200

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gatacgtcag tatgtgttac aggtgatctt ctccgtgacg ttgcatttt 300



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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe	20	25	30	
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser	35	40	45	
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe	50	55	60	
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp	65	70	75	
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val	80	85	90	
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu	95	100	105	
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe	110	115	120	
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135	
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150	
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165	
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180	
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln				

	185		190		195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala		
	200		205		210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser		
	215		220		225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly		
	230		235		240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu		
	245		250		255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala		
	260		265		270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr		
	275		280		285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys		
	290		295		300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys		
	305		310		315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu		
	320		325		330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe		
	335		340		345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu		
	350		355		360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser		
	365		370		375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr		
	380		385		390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu		
	395		400		405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn		
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Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu		
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Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu		
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Lys Gln Met Ala	Pro				
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<211> 407  
<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 78, 81, 113, 157, 224, 297  
<223> unknown base

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tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350  
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400  
tttcag 407

<210> 432  
<211> 457  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434  
<223> unknown base

<400> 432  
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tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400  
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tggtgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

ctcgcgagg gatcgccca tggccggggc tcggagccgc gacccttggg 50

gggcctccgg gatttgctac ctttttggtt ccctgctcgt cgaactgctc 100

ttctcacggg ctgtcgctt caatctggac gtgatgggtg ccttgcgcaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

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a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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				20					25					30

Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45

Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90

Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105



Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu
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Asn Gln Trp Leu	Gly Val Ser Val Arg Ser	Gln Gly Pro Gly Gly
125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val
140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val
155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu
170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly
185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His
200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr
215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His
230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp
245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser
260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe
275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile
290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu
305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val
320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala
335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr
350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu
365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala
380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	950	955	960

Cys Val Val Phe	Ser Cys Pro Leu Tyr	Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val	Trp Gly Arg Leu Trp Asn	Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala	Val Lys Ser Leu Glu Val	Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys	Ser Ser Ile Lys Asn Leu	Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile	Pro Val Met Val Tyr Leu	Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly	Val Pro Trp Trp Val Ile	Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu	Val Leu Ala Leu Leu Val	Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe	Lys Arg Ala Lys His Pro	Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala	Val Lys Ile Pro Arg Glu	Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys	Thr Gly Thr Ile Leu Arg	Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu	Gly Pro Asp Ala His Pro	Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu	Leu Gly Pro Asp Gly His	Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150  
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200  
ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250  
gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300  
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350  
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gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950  
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 aattcttgatg acacatacaa ggacagtta atatctaata atgagtgggtg 1050  
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 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250  
 gaataaatgg tgttgcagat tgtgctatag attttgagat ctccggagat 1300  
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 cctatttaaa attatcttct tccccaataa caaaatgatt ctaaacctca 1550  
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 aattctaagt gaaatttaaa ataaataaat ttttaatgac ctgggtctta 1850  
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900  
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
 aaaaaaaaaa aaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp
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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20				25						30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	Leu Cys Asp Glu Asp Gly	
335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly	Ser Val Gly Gln Cys Trp	
350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val	Met Gly Ser Arg Ile Asn	
365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe	Glu Ile Ser Gly Asp Phe	
380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr	Asp Asp Glu Asp Asp Glu	
395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu	Ile Glu Asp Asp Asp Glu	
410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly	Asp Asp His Asp Val Tyr	
425	430	435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445



ggttactaca agccaacaca atgtcatggc agtgttgagc agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100

cagggatggg cgacaagatc tggctgccct tccccgtgct ctttctggcc 150

gctctgcctc cgggtgctgt gcctggggcg gccggcttca caccttccct 200

cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgttct 250

accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300

gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350

aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400

ctgaagtggg tgattacatg ttctgctttg acaatacatt cagcaccatt 450

tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500

ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550

tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600

agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650

tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700

ctatggttaa tttagtggtc atggtggtgg tgtcagccat tcaagtttat 750

atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800

caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850

tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900

aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950

tgtgcaagta atcctgctga tccagttgta cttaagtgtg taacaggaat 1000

attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050

tttcctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100

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 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

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<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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gccctgcca gtgtgtcctg gatgctgctt tctgacctca ttctcctgtg 150  
tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200  
gctgtcccaa aggetccaag gcctatggct cccctgcta tgccttgttt 250  
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300  
ctctggaaaa ctggtgtctg tgctcagtgg ggctgagga tccttcgtgt 350  
cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400  
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
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ttcctttttt ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800  
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aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT

<213> Homo sapiens

<400> 452

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
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Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
20 25 30

Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
35 40 45

Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser  
50 55 60

Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys  
65 70 75

Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser  
80 85 90

Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly  
95 100 105

Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp  
110 115 120

Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys  
125 130 135

Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser  
140 145 150

Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala  
155 160 165

Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp  
170 175

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

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tgcgctgcta cgtctgtccg gagcccacag gagtgtcgga ctgtgtcacc 200

atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250

ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400  
 tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
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<210> 454  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 454  
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 Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
                     20                    25                    30  
 Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
                     35                    40                    45  
 Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
                     50                    55                    60  
 Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
                     65                    70                    75  
 Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
                     80                    85                    90  
 Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
                     95                    100                    105  
 Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
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 Leu Ser Leu Arg Leu  
                     125

<210> 455  
 <211> 1518  
 <212> DNA  
 <213> Homo sapiens

<400> 455  
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 attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150  
 gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250  
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 acccaggctc tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caactaccag ccgtaccctg gcgcagagga 400  
 cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcggagggg 450  
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 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
 ccttcatcaa ctcaatccta aggatataca agttctgtgg ttccagttaa 1050  
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 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
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 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266



<212> PRT

<213> Homo sapiens

<400> 456

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				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
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<211> 638  
<212> DNA  
<213> Homo sapiens

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509, 556  
<223> unknown base

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<210> 458  
<211> 4040  
<212> DNA  
<213> Homo sapiens

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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	

Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly	200	205	210
Met	Ala	Pro	Val	Lys	Tyr	His	Gly	Asp	Arg	Ser	Lys	Glu	Ser	Leu	215	220	225
Val	Ser	Phe	Ala	Met	Gln	His	Val	Arg	Ser	Thr	Val	Thr	Glu	Leu	230	235	240
Trp	Thr	Gly	Asn	Phe	Val	Asn	Ser	Ile	Gln	Thr	Ala	Phe	Ala	Ala	245	250	255
Gly	Ile	Gly	Trp	Leu	Ile	Thr	Phe	Cys	Ser	Lys	Gly	Gly	Asp	Cys	260	265	270
Leu	Thr	Ser	Gln	Thr	Arg	Leu	Arg	Leu	Ser	Gly	Met	Leu	Phe	Leu	275	280	285
Asn	Ser	Leu	Asp	Ala	Lys	Glu	Ile	Tyr	Leu	Glu	Val	Ile	His	Asn	290	295	300
Leu	Pro	Asp	Phe	Glu	Leu	Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg	305	310	315
Leu	Ala	His	His	Arg	Trp	Leu	Leu	Phe	Phe	His	Phe	Gly	Lys	Asn	320	325	330
Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Leu	Lys	Thr	Leu	Leu	335	340	345
Lys	Asn	Asp	His	Ile	Gln	Val	Gly	Arg	Phe	Asp	Cys	Ser	Ser	Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	650	655	660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	665	670	675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	680	685	690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	695	700	705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	710	715	720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	725	730	735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				740	745	

<210> 460  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 460  
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<210> 461  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 461  
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<210> 462  
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<210> 463  
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 <212> DNA



<213> Homo sapiens

<400> 463

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<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

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Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly			

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly	His Glu Gly Ile Pro	
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe	Ala Ala Val Gly Phe	
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala	Leu Gly Lys Thr Gly	
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe	Val Asn Thr Gly Phe	
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro	Val Leu Glu Thr Asp	
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile	Leu Thr Asn Lys Lys	
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile	Phe Leu Arg Leu Gln	
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile	Leu Asn Arg Met Gln	
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His	Lys Ile Lys Met Lys	
290	295	300

<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250

aggccgcaca cggggccgcc gctgcccacg cccgggcccg acagggacag 300

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gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400

cctgcgcccg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450

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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
				20					25					30
Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45
Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
				50					55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser		65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln		80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp		95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln		110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser		125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro		140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala		155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg		170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro		185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala		200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys		215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys		230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe		245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe		260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro		275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe		290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu		305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His		320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu		335	340	345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
 350 355 360  
 Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
 365 370 375  
 Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
 380 385 390  
 Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
 395 400 405  
 Pro Lys Pro Glu Asn Leu Leu Arg Asp  
 410

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
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 acgggatggc tacgggaacg cgctatgccg ggaaggtggg ggtcgtgacc 150  
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 cggggcccca gtggttatct gcgacaagga tgagtctggg ggccggggcc 250  
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 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400  
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<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

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				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn
				125					130					135
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln
				140					145					150
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr
				155					160					165
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn
				170					175					180
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu
				185					190					195
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met
				200					205					210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
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<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

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 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300  
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 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
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 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
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<210> 470  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
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 20 25 30



Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
				35					40					45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
				155					160					165
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
				170					175					180

<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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cactctccca gcattttttc atgcaaagga tgggatattc cgccgttata 500

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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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			20						25					30
Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
			35						40					45
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
			50						55					60
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
			65						70					75
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
			80						85					90
Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
			95						100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
			110						115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
			125						130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
			140						145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
			155						160					165

Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	
				170					175					180	
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala	
				185					190					195	
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	
				200					205					210	
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	
				215					220					225	
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	
				230					235					240	
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	
				245					250					255	
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	
				260					265					270	
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	
				275					280					285	
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	
				290					295					300	
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	
				305					310					315	
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	
				320					325					330	
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	
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Asp Lys Gly Leu

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 474

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 474

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<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

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<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser	170	175	180	
Val	Ile	Tyr	Asp	Gln	Leu	Cys	Ser	Val	Pro	Ser	Tyr	Ser	Ile	Cys	185	190	195	
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<400> 479  
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<400> 480  
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<210> 481  
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<210> 482  
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<213> Homo sapiens

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<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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				20					25					30

Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35					40					45

Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50					55					60

Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65					70					75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80					85					90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
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Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484  
<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 68, 70, 84, 147  
<223> unknown base

<400> 484  
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cggtgggcct gacaggtctt gaaggctggc tgccgagcca gtgccatctt 200  
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<400> 485  
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<210> 486  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

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<223> unknown base

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly	1	5	10	15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	20	25	30	
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

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<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu	1	5	10	15
Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	20	25	30	
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480

Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	485	490	495
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	500	505	510
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	515	520	525
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	530	535	540
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	545	550	555
Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val	560	565	570
Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	575	580	585
Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	590	595	600
Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr	605	610	615
Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His	620	625	630
Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	Leu	635	640	645
Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn	650	655	660
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro	665	670	675
Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe	680	685	690
Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	695	700	705
Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	710	715	720
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	725	730	735
Arg	Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	740	745	750
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	755	760	765



Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

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<212> DNA  
<213> Homo sapiens

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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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				20					25					30
Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45
Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60
Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75
Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90
Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105
Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
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Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135
Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150
Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165
Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180
Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195
Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210
Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225
Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340	345
Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser
350	355	360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg
365	370	375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu
380	385	390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe
395	400	405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu
410	415	420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys
425	430	435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His
440	445	450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser
455	460	465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala
470	475	480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe
485	490	495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu
500	505	510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu
515	520	525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
Asp Ser Ile Lys Gln Tyr	1040		

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



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<210> 500  
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<223> Synthetic oligonucleotide probe

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<210> 505  
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<213> Homo sapiens

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<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

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				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu

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Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys	260		265		270

Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
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Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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ctgaggcccc agcaagggct aggggtccatc tccagtccca ggacacagca 150  
gcggccacca tggccacgcc tgggtccag cagcatcagc agcccccagg 200  
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ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240



Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

tgagcagca atatgccagc c 21

<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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agttgggtct ccgtgtttca ggccggctcc cccttctctg tctcccttct 200  
cccgtgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350  
cattttggag caggaattcc aatcatgtct gtgatgggtg tgagaaagaa 400  
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atggccgct catgatggcc cggcaaaagg gcattttcta cctgaccctt 500  
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305		310		315
Glu Thr Ser Ser	Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr	Glu		
	320	325	330		
His Leu Asn Ser	Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro	Glu		
	335	340	345		
Glu Met Pro Pro	Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala	Ala		
	350	355	360		

Glu Ala Glu Lys

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 tttggctttg gactctcnct ttctcccaca gagcncttcg accatcactg 150  
 ccctggggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcactct ttntctctcc cncctcaca totatgtctt cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 517  
 caacgtgatt tcaaagctgg gctc 24

<210> 518  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<210> 521

<211> 50

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<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccacctcag 300

gtgcactatt gacaaccggg tcaccgggt ggctggcta aaccgcagca 350

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cttctgagca acacccaaac gcagtacagc atcgagatcc agaactgtga 450  
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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
				140					145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	



Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys  
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
305 310 315

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Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
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Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
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Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
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Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
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Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

<400> 613  
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aaataagaaa atttctcaagg aggacgagct cttgagttag acccaacaag 150  
ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250  
cctgatcctg ctcaccgtg gcgctgggct gctggtggc caagttctga 300  
atctgcaggc ggggctccg gtccctggaga tgtatttct caatgacact 350  
ctggcggtg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400  
tggagaacac ctggctcagg gtgcacgag gctgcaagtc ctgcaggccc 450  
aactcacctg ggtccgctc agccatgagc acttgctgca gcgggtagac 500  
aacttcactc agaaccagg gatgttcaga atcaaagggt aacaaggcgc 550  
cccaggctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600  
gcccgcggg accacctgct gagaaggag ccaaggggc tatgggacga 650  
gatggagcaa caggccctc gggaccccaa ggccaccg gatgcaagg 700  
agaggcggc ctccaaggac ccagggtgc tccagggaag caaggagcca 750  
ctggcaccac aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800  
ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850  
gggtctcca ggaagcaaag gggacaggg catgaaagg gatgcaggg 900  
tcatggggc tcctggagc caggggagta aaggtgactt cgggaggcca 950  
ggccaccag gtttggtggt ttttctgga gctaaaggag atcaaggaca 1000  
acctggactg cagggtgttc cggccctcc tggtagctg ggacaccag 1050  
gtgccaagg tgagcctggc agtctggct cccctggcg agcaggactt 1100  
ccaggagcc cgggagtc aggagccaca ggcctgaaag gaagcaaagg 1150  
ggacacagga cttcaaggac agcaaggaag aaaaggagaa tcaggagtgc 1200  
caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcagg 1250  
cccaaggag cccctggaca agctggccag aaggagacc agggagtga 1300  
aggatcttct ggggagcaag gagtaaagg agaaaaagg gaaagagggt 1350  
aaaactcagt gtccgtcagg attgtcggc gtagtaacc aggccgggt 1400  
gaagtttact acagtggtag ctgggggaca atttgcgat acgagtggca 1450

aaattctgat gccattgtct tctgccgcat gctgggttac tccaaaggaa 1500  
 gggccctgta caaagtggga gctggcactg ggcagatctg gctggataat 1550  
 gttcagtgtc ggggcacgga gaggaccctg tggagctgca ccaagaatag 1600  
 ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtga 1650  
 gcgtctgacc cggaaccct ttcacttctc tgctcccgag gtgtcctcgg 1700  
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 tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

Met	Arg	Asn	Lys	Lys	Ile	Leu	Lys	Glu	Asp	Glu	Leu	Leu	Ser	Glu	1	5	10	15
Thr	Gln	Gln	Ala	Ala	Phe	His	Gln	Ile	Ala	Met	Glu	Pro	Phe	Glu	20	25	30	
Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				



185										190				195			
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln			
				200					205					210			
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln			
				215					220					225			
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys			
				230					235					240			
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro			
				245					250					255			
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met			
				260					265					270			
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro			
				275					280					285			
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln			
				290					295					300			
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val			
				305					310					315			
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			
				320					325					330			
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr			
				335					340					345			
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln			
				350					355					360			
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys			
				365					370					375			
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro			
				380					385					390			
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser			
				395					400					405			
Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn			
				410					415					420			
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala			
				425					430					435			
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu			
				440					445					450			
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr			
				455					460					465			
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln			

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

<210> 615  
 <211> 647  
 <212> DNA  
 <213> Homo Sapien

<400> 615  
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 agcacctcct ctcttctcct tttgccccaa ctcacccagt gagtgtgagc 100  
 atttaagaag catcctctgc caagaccaa aggaaagaag aaaaagggcc 150  
 aaaagccaaa atgaaactga tggtaactgt tttcaccatt gggctaactt 200  
 tgctgctagg agttcaagcc atgcctgcaa atcgctctc ttgctacaga 250  
 aagatactaa aagatcaca ctgtcacaac cttccggaag gagtagctga 300  
 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400  
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaaca 450  
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttcccac 500  
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550  
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaactctgt 600  
 gttaaacaag tagtaataaa agttaattca atctaaaaa aaaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616	
Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu	
1 5 10 15	
Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg	
20 25 30	
Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val	
35 40 45	

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617  
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 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100  
 accccgccgt ggtggttga gggcgcgag tagagcagca gcacaggcgc 150  
 ggggtccggg aggccggctc tgctcgcc gagatgtgga atctccttca 200  
 cgaaaccgac tcggctgtgg ccaccgcgc cgcgccgcg tggctgtgcg 250  
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcg cttcctcttc 300  
 ggggtggtta taaaatctc caatgaagct actaacatta ctccaaagca 350  
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400  
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450  
 tttcagcttg caaagcaaatt tcaatcccag tggaaagaat ttggcctgga 500  
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550  
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600  
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650  
 tattgtacca ctttccagt ctttctctcc tcaaggaatg ccagagggcg 700  
 atctagtgtg tgtaactat gcacgaactg aagacttctt taaattggaa 750  
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800  
 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcaggggcca 850  
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 aagtcctatc cagacgggtg gaatcttctt ggaggtggtg tccagcgtgg 950

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cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050  
ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100  
agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150  
tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa cttttctaca 1200  
caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350  
agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400  
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cagaagaatt tggctcttctt ggttctactg agtgggcaga ggagaattca 1500  
agactccttc aagagcgtgg cgtggcttat attaatgctg actcatctat 1550  
agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600  
tggtacacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650  
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aattgggaaa caaacaatt cagcggctat ccactgtatc acagtgtcta 1850  
tgaaacatat gagttggtgg aaaagtttta tgatccaatg tttaaatata 1900  
acctcactgt ggcccagggt cgaggaggga tgggtgtttga gctagccaat 1950  
tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000  
gtatgctgac aaaatctaca gtatttctat gaaacatcca caggaaatga 2050  
agacatacag tgtatcattt gattcacttt tttctgcagt aaagaatttt 2100  
acagaaattg cttccaagtt cagtgaagaga ctccaggact ttgacaaaag 2150  
caaccctaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200  
gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250  
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300  
aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350  
aggcctgggg agaagtgaag agacagattt atgttcagc cttcacagt 2400

caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450  
 gaatccgtat tgaatttggtg tggatatgtca ctcagaaaga atcgtaatgg 2500  
 gtatatgtat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550  
 atatataa 2558

<210> 618  
 <211> 750  
 <212> PRT  
 <213> Homo Sapien

<400> 618  
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 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly  
 20 25 30  
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser  
 35 40 45  
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala  
 50 55 60  
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His  
 65 70 75  
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe  
 80 85 90  
 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu  
 95 100 105  
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro  
 110 115 120  
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly  
 125 130 135  
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly  
 140 145 150  
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser  
 155 160 165  
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala  
 170 175 180  
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn  
 185 190 195  
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg  
 200 205 210

Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggtta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe



**BEST AVAILABLE COPY**

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50